


BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...SEQ ID NO: 1Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

42571

Description

None

Molecule type

nucleic acid

Subject Length

20

ProgramBLASTN 2.2.20+ [Citation](#)**Reference**Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hittist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Filter string Lm;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

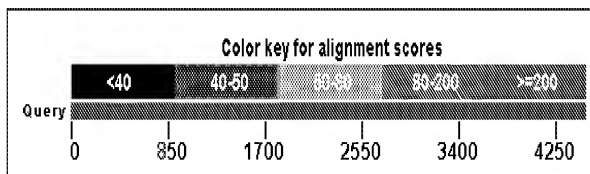
Effective search space 44750

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#)

Plot of gi|11545911|ref|NM_022162.1| vs 42571

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



[Descriptions](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

42571	37.4	37.4	0%	3e-07	100%
-------	------	------	----	-------	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>lcl|42571
Length=20

Score = 37.4 bits (40), Expect = 3e-07
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query	2134	TTCCTGGCAGGGCTGTTGTC	2153
Sbjct	1	TTCCTGGCAGGGCTGTTGTC	20

[Select All](#) [Get selected sequences](#) [Distance tree of results](#)


BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...SEQ ID NO: 2

Results for: ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

1677

Description

None

Molecule type

nucleic acid

Subject Length

20

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hittist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Filter string Lm;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

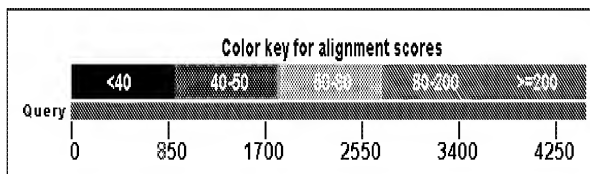
Effective search space 44750

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#)

Plot of gi|11545911|ref|NM_022162.1| vs 1677

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



[Descriptions](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

1677	37.4	37.4	0%	3e-07	100%
------	------	------	----	-------	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>lcl|1677
Length=20

Score = 37.4 bits (40), Expect = 3e-07
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query	2247	CCTCCGCAAGCACTTCCACT	2266
Sbjct	20	CCTCCGCAAGCACTTCCACT	1

[Select All](#) [Get selected sequences](#) [Distance tree of results](#)

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...SEQ ID NO:5

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

26991

Description

None

Molecule type

nucleic acid

Subject Length

26

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hittlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1
Template length	18
Window Size	40

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 67110

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

[Descriptions](#)


[Alignments](#)

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...SEQ ID NO:6

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

17521

Description

None

Molecule type

nucleic acid

Subject Length

20

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hittist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Filter string Lm;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

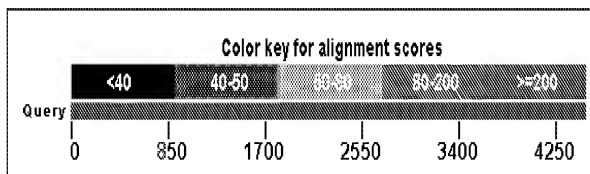
Effective search space 44750

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#)

Plot of gi|11545911|ref|NM_022162.1| vs 17521

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



[Descriptions](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

17521	37.4	37.4	0%	3e-07	100%
-------	------	------	----	-------	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>lcl|17521
Length=20

Score = 37.4 bits (40), Expect = 3e-07
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query	2881	CACCAGAGCTTGAGGTGGCT	2900
Sbjct	20	CACCAGAGCTTGAGGTGGCT	1

[Select All](#) [Get selected sequences](#) [Distance tree of results](#)


BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...SEQ ID NO:9

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

53501

Description

None

Molecule type

nucleic acid

Subject Length

26

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hittist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Filter string Lm;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

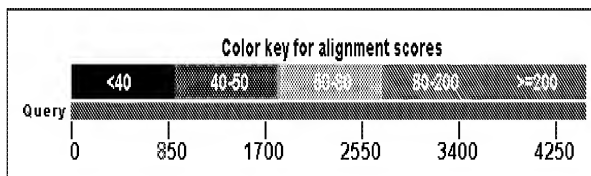
Effective search space 67110

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#)

Plot of gi|11545911|ref|NM_022162.1| vs 53501

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



[Descriptions](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

53501	48.2	48.2	0%	2e-10	100%
-------	------	------	----	-------	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>lcl|53501
Length=26

Score = 48.2 bits (52), Expect = 2e-10
Identities = 26/26 (100%), Gaps = 0/26 (0%)
Strand=Plus/Plus

Query	3075	GTCCAATAACTGCATCACCTACCTAG	3100
Sbjct	1	GTCCAATAACTGCATCACCTACCTAG	26

[Select All](#) [Get selected sequences](#) [Distance tree of results](#)


BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...SEQ ID NO:10

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

691

Description

None

Molecule type

nucleic acid

Subject Length

24

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hittist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Filter string Lm;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

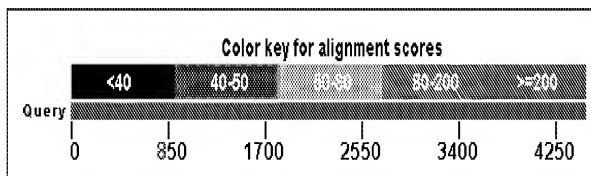
Effective search space 62650

Graphic Summary

Distribution of 2 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#)

Plot of gi|11545911|ref|NM_022162.1| vs 691

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

691	37.4	60.3	0%	4e-07	100%
-----	------	------	----	-------	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>lcl|691
Length=24

Sort alignments for this subject sequence by:
E value **Score** **Percent identity**
Query start position **Subject start position**

Score = 37.4 bits (40), Expect = 4e-07
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query	3137	ACACCATCCTGGAAGTCTGG	3156
Sbjct	24	ACACCATCCTGGAAGTCTGG	5

Score = 22.9 bits (24), Expect = 0.008
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query	1065	AGACTTCCAGGA	1076
Sbjct	7	AGACTTCCAGGA	18

[Select All](#) [Get selected sequences](#) [Distance tree of results](#)